

Fig. 1A

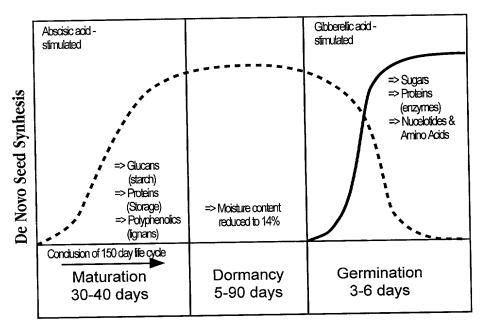


Fig. 1B

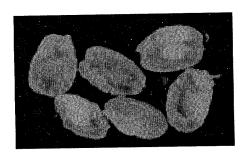


Fig. 1C

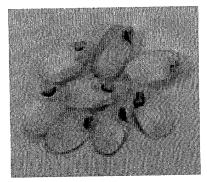


Fig. 1D

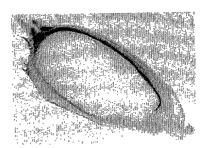


Fig. 1E

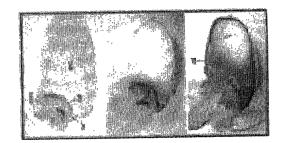


Fig. 1F



Fig. 2A

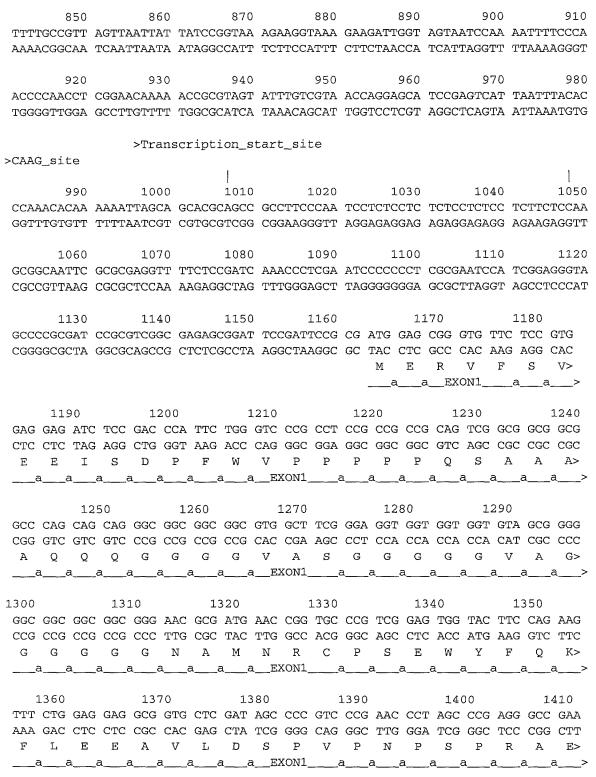


Fig. 2B

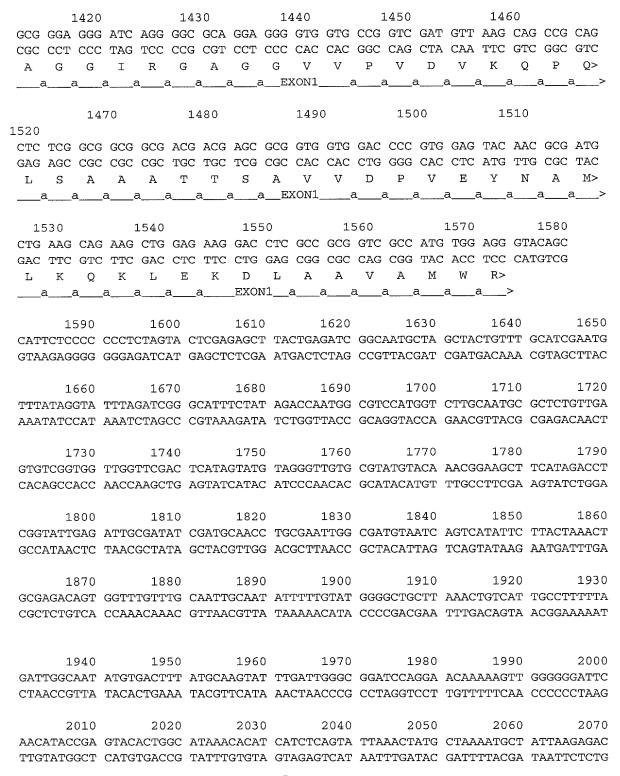


Fig. 2C

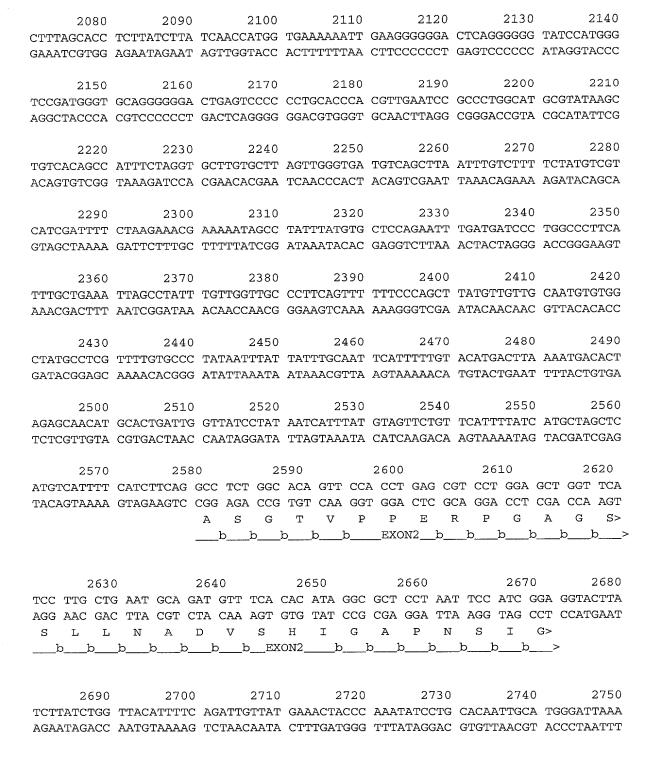


Fig. 2D

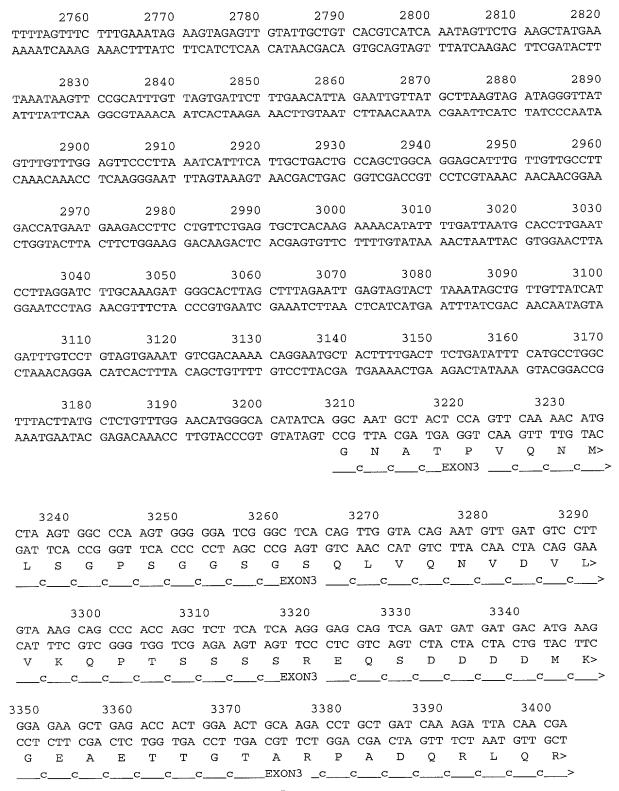


Fig. 2E

AGGTGATC ATTCATTGCT TCCTTGTAAT ATAGATTCTG TACATAATTA ACCTACCTCG TCATGCATGC TCCACTAG TAAGTAACGA AGGAACATTA TATCTAAGAC ATGTATTAAT TGGATGGAGC AGTACGTACG ATGTGTCCTA TTTTCACCTT AGCCCTTTCA GTTGGATTTC CACTTTCATC CGGTAGCCTT TCAGTTTCCT TACACAGGAT AAAAGTGGAA TCGGGAAAGT CAACCTAAAG GTGAAAGTAG GCCATCGGAA AGTCAAAGGA ATTGCATCGC ATATATGATC TTTTACCTAC CATATTAGTT CTCTGTGTGC CATACTCAGT GCTTAGTGTC TAACGTAGCG TATATACTAG AAAATGGATG GTATAATCAA GAGACACACG GTATGAGTCA CGAATCACAG TCGAGCAAGA GAGGAATTTG TATGGCTATT ACACGTAGCA CTTTGCTCTC TACTTGTTTA TTGACATAAG AGCTCGTTCT CTCCTTAAAC ATACCGATAA TGTGCATCGT GAAACGAGAG ATGAACAAAT AACTGTATTC CAATTTGGGA TGAATTAAAT CTGAGTTCAC ATCATATTCC TTATGTCACA AGTTTCTGAA ACCGATTGTA GTTAAACCCT ACTTAATTTA GACTCAAGTG TAGTATAAGG AATACAGTGT TCAAAGACTT TGGCTAACAT TCTAGTATCT GGTTGATGCA CCCCCATCTT GGATTTGCAA ATCAAAGTTA TACTCCCTAG AGAGCTTTAC AGATCATAGA CCAACTACGT GGGGGTAGAA CCTAAACGTT TAGTTTCAAT ATGAGGGATC TCTCGAAATG CTTTCATAAA GCAATTACCC CAATAAACCA CGGATTTGAT AGCTATTGAC TATGATTACC AGAATTCATT GAAAGTATTT CGTTAATGGG GTTATTTGGT GCCTAAACTA TCGATAACTG ATACTAATGG TCTTAAGTAA TGGCAGCTAT TTTCTCAATT TAAGTTTGGT ATTAGTCTCA GTTGGCTGTA AAATAATGTC ACGGTAGGGT ACCGTCGATA AAAGAGTTAA ATTCAAACCA TAATCAGAGT CAACCGACAT TTTATTACAG TGCCATCCCA ACATGTATGT GCAGCATACA AGGTATGGGT GAGTTATGAT ATGGACAGTG TGTACACCCC ACATTTGCTC TGTACATACA CGTCGTATGT TCCATACCCA CTCAATACTA TACCTGTCAC ACATGTGGGG TGTAAACGAG ACTAAAATCA AAATATTCAA ACGTCACGTG ATGATATGGT GGATTGCATT ATACCTTGTA TTGTTTATTA TGATTTTAGT TTTATAAGTT TGCAGTGCAC TACTATACCA CCTAACGTAA TATGGAACAT AACAAATAAT TGTTACTTGT GCTAGACAAT AATATAGGCT GTTCTTTTGG GTGATTTTGT ATGAAGATGT TGAGCAAGCA ACAATGAACA CGATCTGTTA TTATATCCGA CAAGAAAACC CACTAAAACA TACTTCTACA ACTCGTTCGT CTTCTCGATA TAATGCTAGT TTTGTTGACC TGTTCC AGG AAG CAA TCC AAT CGG GAG TCA GCC GAAGAGCTAT ATTACGATCA AAACAACTGG ACAAGG TCC TTC GTT AGG TTA GCC CTC AGT CGG Ν K Q S R

Fig. 2F

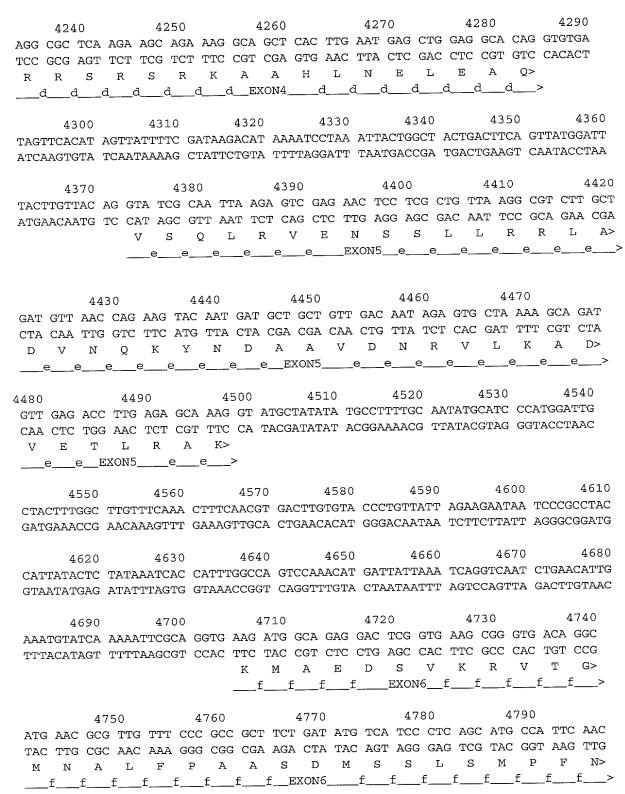


Fig. 2G

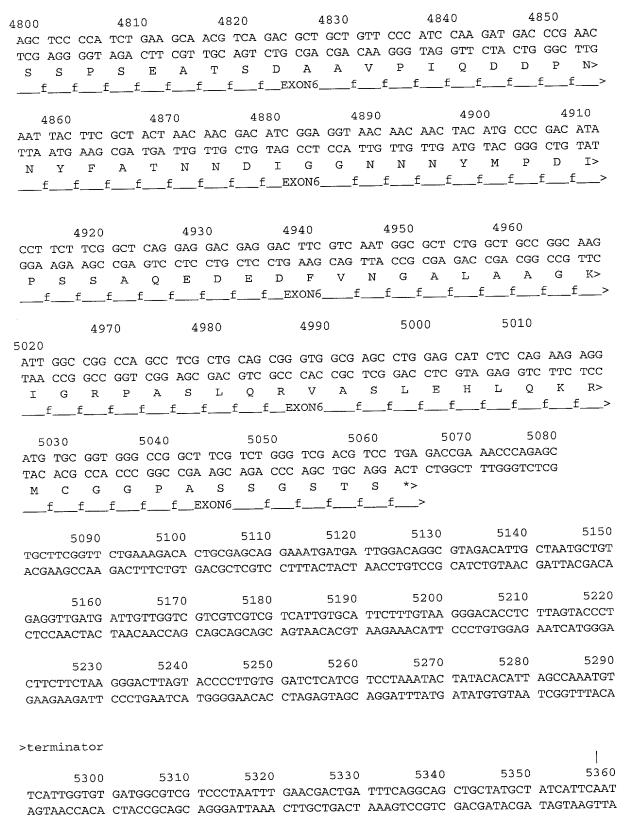


Fig. 2H

E270	5380	5390	5400	5410	5420	5430
5370	TCGATGCTTC				ATAAAGATAT	CACTACCTTT
THE THE PART OF TH	AGCTACGAAG	GAGAACAGAA	AACGAGAATT	CGTTGGTTCG	TATTTCTATA	GTGATGGAAA
TIATAAACT	Ademedias	01101110110111				
5440	5450	5460	5470	5480	5490	5500
TGAGCTGTTC	ATTTGAAGTG	CAAAGCTAAG	CTCAATATCT	CAGGTGTTCA	TTTGAAGTTT	AAAGGTGAAC
ACTCGACAAG	TAAACTTCAC	GTTTCGATTC	GAGTTATAGA	GTCCACAAGT	AAACTTCAAA	TTTCCACTTG
5510	5520	5530	5540	5550	5560	5570
TGATAACAAA	CGTCAGGCTA	TGGTGAATGA	AGGGACGTGT	ACATCCCTAA	TACATGTCAT	TTTCATAATC
ACTATTGTTT	GCAGTCCGAT	ACCACTTACT	TCCCTGCACA	TGTAGGGATT	ATGTACAGTA	AAAGTATTAG
						5640
5580	5590	5600	5610	5620	5630	5640
AAATTAGTTG	ATGCATTTTC	ACCCAGAATC	CCATCACAGT	TCATCATACA	AGCAAGTGTA	GTTATTAATG
TTTAATCAAC	TACGTAAAAG	TGGGTCTTAG	GGTAGTGTCA	AGTAGTATGT	TCGTTCACAT	CAATAATTAC
				= 500	F700	5710
5650	5660	5670	5680	5690	5700	
GTAAATTTTT	CGTTTAGAGA	AAAAAAAAGG	AAGCCTTATA	TAAGATTCAC	CGGTGGGGTG	TGAACAATAA
CATTTAAAAA	GCAAATCTCT	TTTTTTTTCC	TTCGGAATAT	ATTCTAAGTG	GCCACCCCAC	ACTIGITATI
==0.0	EE 2.0	E740	5750	5760	5770	5780
5720	5730 AGATCGCATC	5740			=	
TCAATGAATG	TCTAGCGTAG	CCGTAAGGGC	TCCCATCCAT	CTCTTTTTAC	GTATTTTGAG	GCATATGGTT
AGTTACTTAC	TCTAGCGTAG	GGCATTCCCG	ICGGAICGAI	CIGITITIAC	011111110110	0011111
F700	5800	5810	5820	5830	5840	5850
5790	GCTTGCGCAC				CGCGGGCAAG	AAACGAATCA
CCACAACAAC	CGAACGCGTG	CCCCACTTTA	CCGTCGCTGA	AGTAGCGAAA	GCGCCCGTTC	TTTGCTTAGT
GGTGTTGTTG	CGAACGCGIG	CGCG23C11111	00010001011			
5860	5870	5880	5890	5900	5910	5920
AGTGATACAT	TGGCAGGGAA	CCACCAAAAG	AAGGCCATCC	AATCCAATCC	ACTCCAACGC	GGCATGGAAG
TCACTATGTA	ACCGTCCCTT	GGTGGTTTTC	TTCCGGTAGG	TTAGGTTAGG	TGAGGTTGCG	CCGTACCTTC
5930	5940	5950	5960			5990
ACAAGACAGA	TGATTCACAG	CTATCTTCTG	CTTCTACAAG	TTTGATACTT	TGTACTGTCC	TTTCAGGGAA
TGTTCTGTCT	ACTAAGTGTC	GATAGAAGAC	GAAGATGTTC	AAACTATGAA	ACATGACAGG	AAAGTCCCTT
6000	6010	6020	6030			
AAAAGAGCAT	CAGATTAGTC	TGATCTCGGG	CGCGTTGAGT	TCTTGTGGGA	GATCTTGTTG	TGGAGTGGCA
TTTTCTCGTA	GTCTAATCAG	ACTAGAGCCC	GCGCAACTCA	AGAACACCCT	CTAGAACAAC	ACCTCACCGT
				5440	6100	6130
6070						
GGAGTGACGA	. TCGGCTGCCC	CGTTTTCTTC	TACCGAAACA	TCGCCAGTAA	AGAAGCCAAA	AAGACAATAA
CCTCACTGCT	AGCCGACGGG	GCAAAAGAAG	ATGGCTTTGT	AGCGGTCATI	1011099171	TICIGITALL
مندم		6160	6170	6180	6190	6200
6140						GAATGACATG
TACGGCAATG	GGGATCGCCC	MYCYCCMYMM AICIGCHIAA	, 4404110041	. GACGGAACIC	ТААТТАТОТ	CTTACTGTAC
ATGCCGTTAC	, CCCTAGCGGG	IAGACGIATI	TIGIAACGIA	CIGCCIIOAC		3=====
6210	6220					
	OZZO A ATTACGCGTG					
	TAATGCGCAC					

Fig. 2I

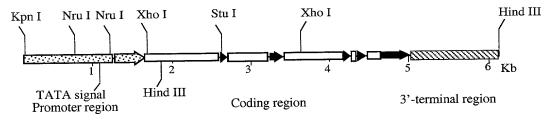


Fig. 3

90 GCCATGTGGC	180 GCCACGTAAG C		270 ccgccgaggg	360 GACAAGTTAA	450 AGGCCTTTT	540 ATTTTCTGCA	630 CAGAGGCAAA	720 ACCAAGAGAA	810 TCCAACCGAT	900 CCCATCCGAT	990 GATCATCAAT		
80 TGATATGTGG	170 GATCGAATT G		260 ACCATCCAAA	350 CAAATTTGTT	440 CTCAAATTAA	530 AGTTACACAC	620 AATCTTTTAT	710 ATTACCCAAC	800 TTGCTCTTT	890 CCTATAAAAC	980 TTGTCTGATT	1060	
70 GGGGTGACAA > Reb_site1	160 TTATTTTCG		250 ccaaaacc	340 GGACGAAAAT	430 TCCAATCCTC	520 CAACATGCGC	610 TACATCCATT	700 AACTTCAGAA	790 CATTGTACTC	880 CCACAAAAAC	970 CTTCTAGTGA	1050	
60 AAGAAGAGA GGGGTGACAA >Reb_site1	150 ATGAGAATTA	b_site2	240 CGCCACGTCAG	330 TTCGATTGAA	420 TCCGTGGGCT	510 TACCAACAAG	600 TTAGTGTAGA	690 CCACATACAT	780 CTCTTTGCAG	870 ACAACCATGG	960 AACATATACA	1040	
50 Agagaggagg	140 TGTGGGTCCC	site1 >reb	230 AGCCACGTAAG	320 TATCTGGTTT	410 GAGCCATATA	500 ACAAAACTAC	590 GACAATCTCA	680 GTGTTATCTG	770 ACCTTTTTCA	860 CACCGTGCAC	950 GAGGAAAAAA	1030	ig. 4
40 AGAGATGGTG	130 GAAACTGACA	>Reb	220 GAGTCAAATT	310 GGACCCGTTG	400 AATATTCTGT	490 CCATAAAAGT	580 TTATCCCTAG	670 TGACACAAAA	760 AATCTTGGAA	850 ACACGAAGCT	940 ACAAACAAAA	site	Έι
30 AGGAGAGGGG	120 TTCTTTTGTT		210 GATGAAGACC	300 GATAGTTGAG	390 TCCATTTCAA	480 TTTCAGTCAC	570 GAGCTAAGAG	660 CAAAAATAGG	750 GCAAGCTCCA	840 TACTTGATCT	930 TTCATCACCA	CAGTCCC	
	110 TTTTAATTCA		200 TGCTACGTCA	290 CACTGGTTTT	380 ATGAACTTAT	460 TAAAATAGAT AATTGCCTTC	550 560 CATTICCACC ACGICACAA	650 CTCTTTATGA	740 AAATCTTTTT	830 CTCAAGCTTC	920 TCATCATCAG	1010 CTAGAGGATC CCCGGGTGGT	
10 20 AAGCTTGCAT GCCTGCAGGG	100 CCCCACCATT		190 GCTACGTCAA	280 ACCTCATCTG	370 GGGACCTTAA	460 TAAAATAGAT	550 CATTTCCACC	640 CGTAAAGCCG	730 АААТААААА АААТСТТ	820 CCATGTCACC	910 CGCCATCATC TCATCAT	1000 CTAGAGGATC	

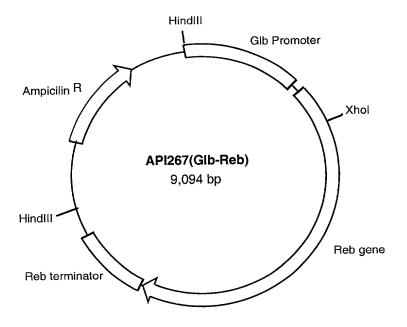


Fig. 5A

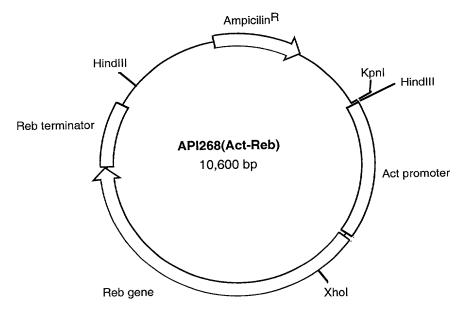
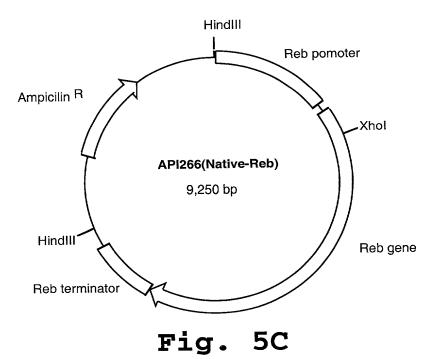
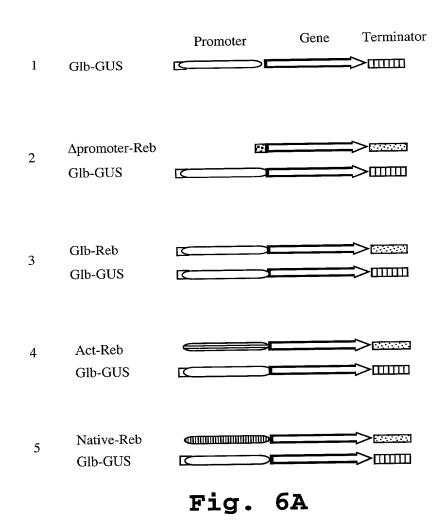


Fig. 5B





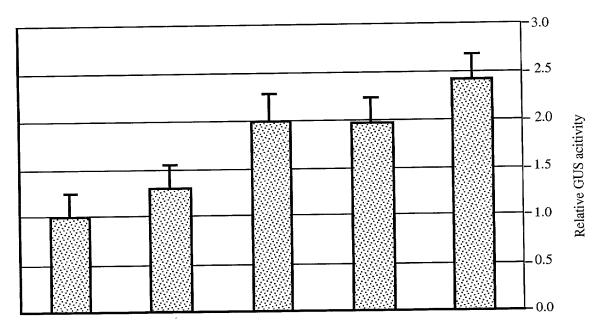
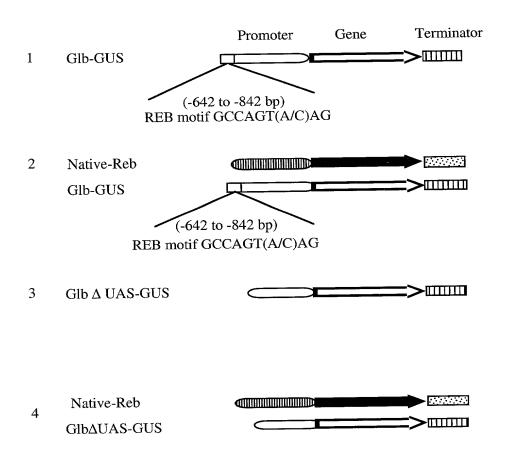
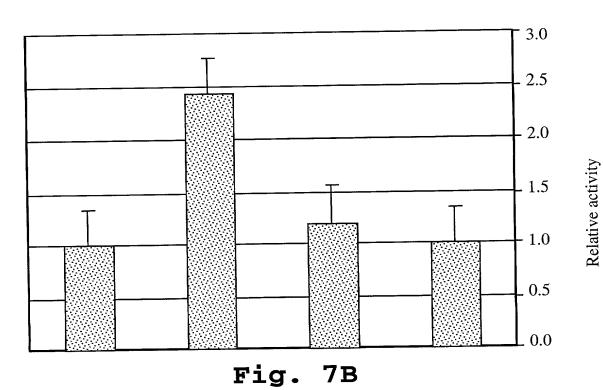


Fig. 6B







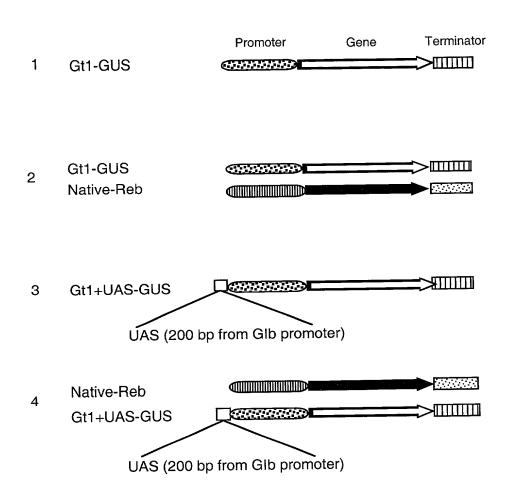
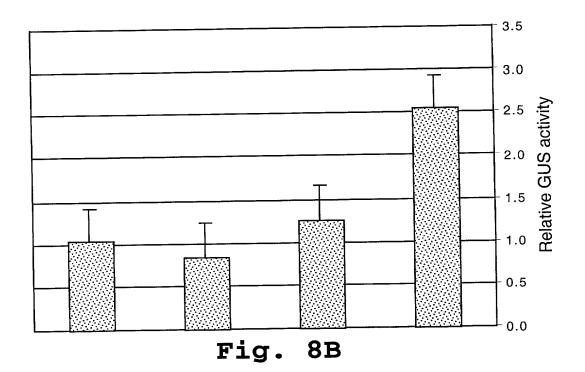


Fig. 8A



10 CTGCAGGGAGGA(20 saggggagaga	30 TGGTGAGAGAC	40 ggaggaagaag	50 AGGAGGGGTG	60 ACAATGATATG1	70 :GGGCCATGTGG	10 20 30 40 50 60 70 80 90 100 CTGCAGGGAGAGAGAAGAAGAAGAAGAAGAGGGGTGACAATGATATGTGGGCCATGTGGCCCCCCCC	100 TAATTCATT
					ACGT core	ACGT core	ACGT core	
110 120 130 140 CTTTTGTTGAAACTGACATGTGGGTCCCATGAGAATTATTAT	120 CTGACATGTGG	130 ggtcccatga <i>gi</i>	.	150 TTCGGATCGA	160 ATTGCC <u>ACGT</u> AA	170 NGCGCT <u>ACGT</u> CA	150 160 170 200 TTCGGATCGAATTGCC <u>ACGT</u> AAGCGCT <u>ACGT</u> CAATGCAGATGAAGACCGA	200 GAAGACCGA
ACGT core	core ACGT	T core						
$\begin{array}{c c} 210 & 220 \\ \hline & 220 \\ \hline & \\ \\ \hline & \\ & \\$	220 <u>ACGT</u> AAGCGCC	ā:l	240 AAACCACCATC	250 CAAACCGCCG	260 AGGGACCTCAT	270 STGCACTGGTTT	230 240 250 260 270 280 290 300 <u>CGT</u> CAGCCAAAACCATCCAAACGCCGCGAGGGACCTCATCTGCACTGGTTTTGATAGTTGAGGGACCCGTTGTA	300 ACCCGTTGTA
310 TCTGGTTTTTCGATTGAAGGA	320 ATTGAAGGACG	330 SAAAATCAAAT	340 TTGTTGACAAG	350 STTAAGGGACC	360 TTAAATGAACT	370 PATTCCATTTCA	330 340 350 360 370 380 390 400 CGAAAATCAAATTTGTTGACAAGTTAAGGGACCTTAAAATGAACTTATTCCATTTCAAAATATTCTGTGAGCCATATATC	400 SCCATATATC
410 CGTGGGCTTCCAATCCTCCTC	420 ATCCTCCTCAA	430 aattaaagggc	440 CTTTTTAAAA1	450 FAGATAATTGC	460 CTTCTTTCAGT	470 CACCCATAAAAG	430 440 450 460 470 480 490 500 AAATTAAAGGGCCTTTTTTAAAATAGATAATTGCCTTCTTTCAGTCACCCATAAAAGTACAAAACTACTACCAACAAGCA	500 SCAACAAGCA
			ACGT core	a				
510 ACATGCGCAGTTACACACATT	520 ACACACATTTI	530 rctgcacattt	$^{ }_{540}$	550 acaaagagct7	 530 540 550 560 570 TTCTGCACATTTCCACA <u>ACGT</u> CACAAAGAGCTAAGAGTTATCCCTAGGACAAT		580 590 600 CTCATTAGTGAGATACATCCATTAA	600 CATCCATTAA
	ACGT cor prole	ore						
 620 TCTTTTATCAGAGGCAA <u>ACGT</u>		630 AAGCCGCTCTT	640 TATGACAAAA	650 ATAGGTGACA0	660 CAAAAGTGTTAT	670 CTGCCACATAC	630 640 650 660 670 680 690 700 <u>NAAAG</u> CCGCTCTTTATGACAAAAATAGGTGACAAAAGTGTTATCTGCCACATACAT	700 TACCCAACAC
					pro	prolaminbox		
710 CAAGAGAAAATAAAAAAAA		730 .TCTTTTTGCAAG	730 TTTGCAAGCTCCAAATCTTGGAAACCT	750 TGGAAACCTT	760 TTTCACT <u>CTTTG</u>	$egin{array}{c} 760 & 770 & 780 \ ext{TTCACTCTTTGCAGCAFTGTACTCTTGCTV} \end{array}$	CTT	790 800 TTTCCAACCGATCC
						TATA_box		
810 ATGTCACCCTCAAGCTTCTAC	820 AGCTTCTACT	830 TGATCTACACG	840 SAAGCTCACCG	850 TGCACACAAC	860 CATGGCCACAAA	870 AACCC <u>TATAAA</u>	830 840 850 860 870 880 890 900 TTGATCTACACGAAGCTCACGACACAACACAAAAAACCCTATAAAAACCCCATCGATCG	900 CCATCATCTC
_start_site								

9

Fig.

10 20 |30 40 50 100 CTGCAGGCCAGGGAAAGACATGGAAAAAGAGGTAGGGCAGGGAAGAACACTTGGAGATCATAGAAGAACATAAGAGGTTAAAACATAGGAGGC prolaminbox prolaminbox

ATAATGGACAATTAAATCTACATTAATTGAACTCATTTAGGGAAGTAAACCAAAATCCATATTCTGG<u>TGTAAAT</u>CAAACTATTTGACGCGGATTTACTAAGA

| 310 320 | 330 340 | 350 360 370 380 390 400 <u>ACGI</u>CATAGATAGATAGATATTG<u>TGAGTTAGATATTGTGAGTCAGGATTTGTGTTGCCTGGAAATCCAACTAAATGACAAGCAACAAA</u> GCN_motif GCN_motif ACGT core

prolaminbox

ACGT core

TTGTTTCTTCTCACGCTTTCTTCATAGGCTAAACTAACCTCGGCGTGCACAACCATGTCCTGAACCTTCACCTCGTCCC<u>1ATAAAA</u>GCCCATCCAACC 880

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Fig. 10

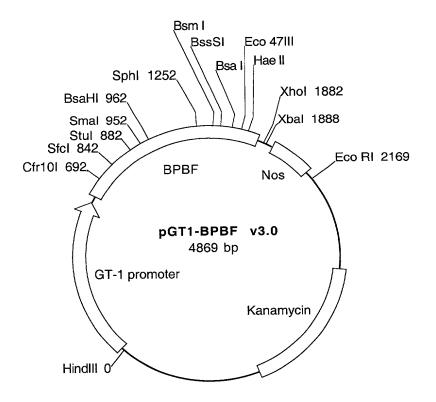


Fig. 11A

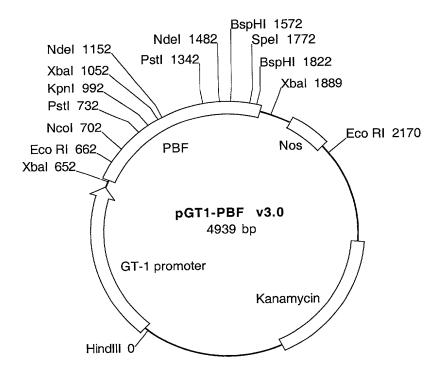


Fig. 11B

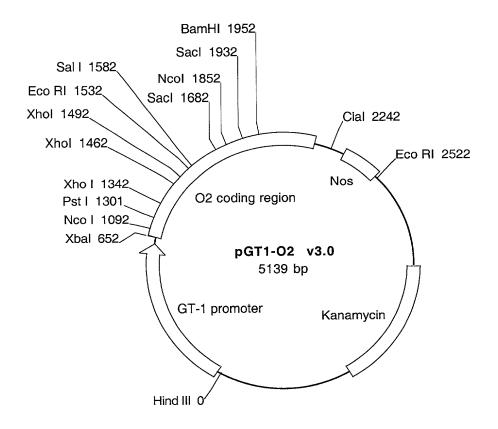


Fig. 11C

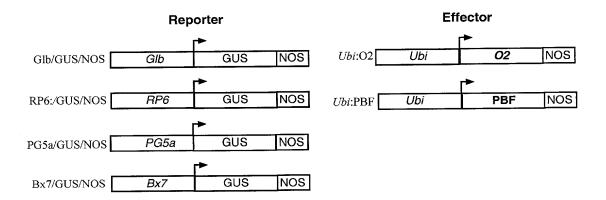


Fig. 12A

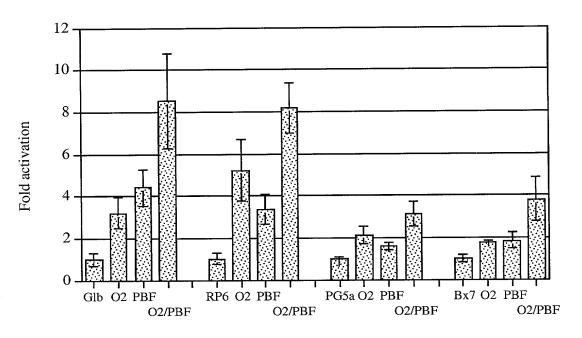


Fig. 12B

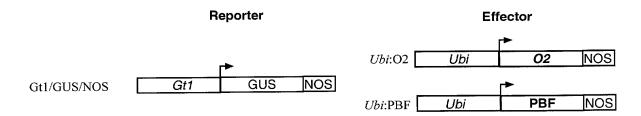


Fig. 13A

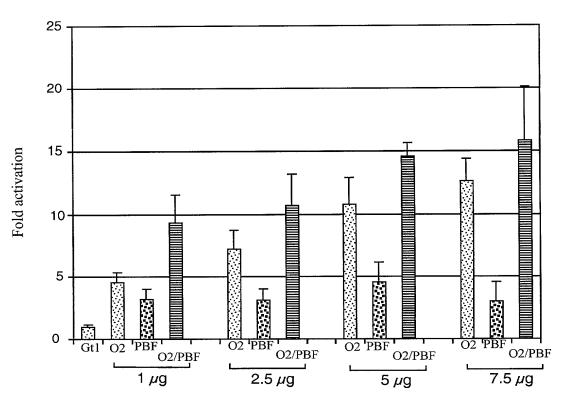


Fig. 13B

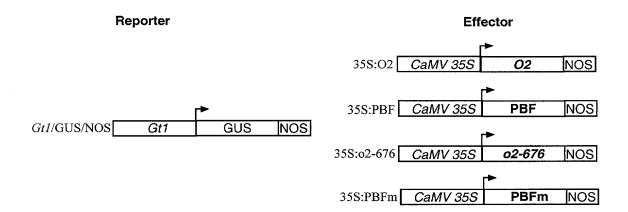
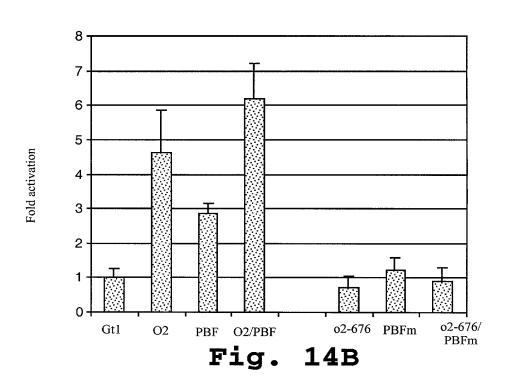


Fig. 14A



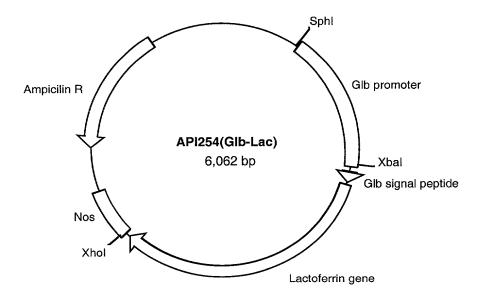


Fig. 15A

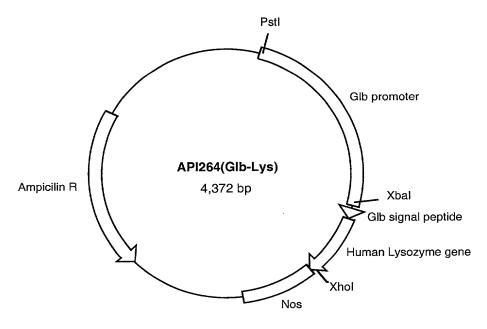


Fig. 15B

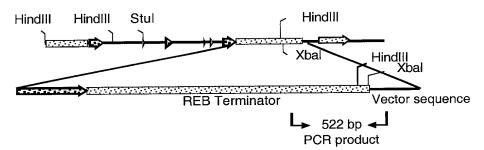


Fig. 16A

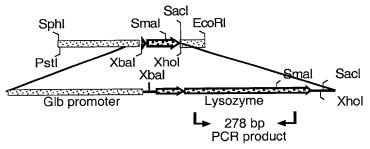


Fig. 16B

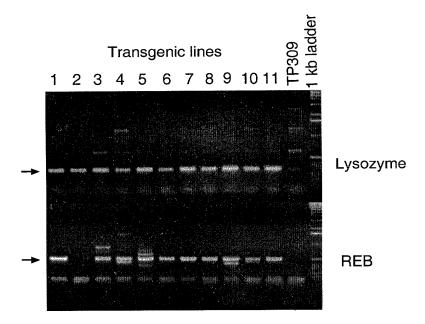


Fig. 16C

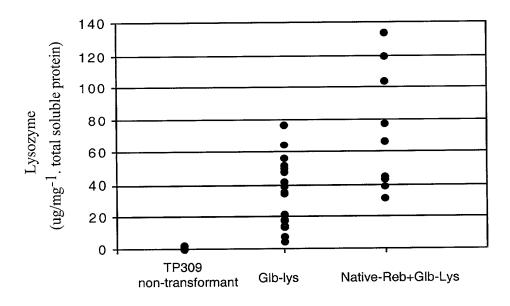


Fig. 17